

TOIG of: a29725 check: 7353 from: 1 to: 1014

Pl:A29725 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30), nuclear - human

N:Alternate names: poly (ADP-ribose) polymerase; poly (ADP-ribose) synthetase;

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A29725; A28498; A39976; A26901; I38096; B33321; A35635; A61559; S14010

R:Uchida, K.; Morita, T.; Sato, T.; Ogura, T.; Yamashita, R.; Noguchi, S.; Suzuki, H.; Nyunoya, H.; Miwa, M.; Sugimura, T.

Biochem. Biophys. Res. Commun. 148, 617-622, 1987

A:Title: Nucleotide sequence of a full-length cDNA for human fibroblast poly(ADP-ribose) polymerase.

A:Reference number: A29725; MUID:88076933

A:Accession: A29725

A:Molecule type: mRNA

A:Residues: 1-69, 'Q', '71-1014 <UCH>

A:Cross-references: GB:M18112; NID:9190166; PIDN:AAA60137.1; PID:g190167

R:Kurosaki, T.; Ushiro, H.; Mitsuuchi, Y.; Suzuki, S.; Matsuda, M.; Matsuda, Y.; Katunuma, N.; Kangawa, K.; Matsuo, H.; Hirose, T.; Inayama, S.; Shizuta, Y.

J. Biol. Chem. 262, 15990-15997, 1987

A:Title: Primary structure of human poly (ADP-ribose) synthetase as deduced from cDNA sequence.

A:Reference number: A28498; MUID:88058958

A:Accession: A28498

A:Molecule type: mRNA

A:Residues: 1-16, 'E', '18-211, 'K', '213-236, 'R', '238-366, 'H', '369-1014 <KUR>

A:Cross-references: GB:J03473

R:Cherney, B.W.; McBride, O.W.; Chen, D.; Alkhatib, H.; Bhatia, K.; Hensley, P.; Smulson, M.E.

Proc. Natl. Acad. Sci. U.S.A. 84, 8370-8374, 1987

A:Title: cDNA sequence, protein structure, and chromosomal location of the human gene for poly(ADP-ribose) polymerase.

A:Reference number: A39976; MUID:88068596

A:Accession: A39976

A:Molecule type: mRNA

A:Residues: 1-49, 'D', '51-612, 'Q', '614-907, 'Y', '909-939, 'R', '941-979, 'I', '981-1014 <CHE>

A:Cross-references: GB:J03030

A:Note: the authors translated the codon ATA for residue 980 as Asn

R:Suzuki, H.; Uchida, K.; Shima, H.; Sato, T.; Okamoto, T.; Kimura, T.; Miwa, M.

Biochem. Biophys. Res. Commun. 146, 403-409, 1987

A:Title: Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and expression of its gene during HL-60 cell differentiation.

A:Reference number: A26901; MUID:87298455

A:Accession: A26901

A:Molecule type: mRNA

A:Residues: 441-610, 'N', '612-880; 921-1014 <SUZ>

A:Note: the sequence figure has an omission of forty residues

R:Ogura, T.; Nyunoya, H.; Takahashi-Masutani, M.; Miwa, M.; Sugimura, T.; Esumi, H.

Biochem. Biophys. Res. Commun. 167, 701-710, 1990

A:Title: Characterization of a putative promoter region of the human poly(ADP-ribose) polymerase gene: structural similarity to that of the DNA polymerase beta gene.

A:Reference number: I38096; MUID:90211250

A:Accession: I38096

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-40 <RES>

A:Cross-references: EMBL:X16674; NID:g510112; PIDN:CAA34663.1; PID:g1017423

R:Auer, B.; Nagl, U.; Herzog, H.; Schneider, R.; Schweiger, M.

DNA 8, 575-580, 1989

A:Title: Human nuclear NAD(+) ADP-ribosyltransferase (polymerizing): organization of the gene.

A:Reference number: A33321; MUID:90091744

A:Accession: B33321

A:Molecule type: DNA

A:Residues:

38-43; 93-98; 132-137; 204-209; 237-242; 276-281; 335-340; 384-389; 431-436; 512-517; 535-540; 580-585; 645-650; 688-693; 716-721; 757-762; 800-805; 833-838; 884-889; 927-932; 947-952; 986-991 <AUE>

A:Cross-references: GB:M29544; GB:M22953

A:Note: the authors translated the codon GTG for residue 54 as Glu

A:Note: these fragments represent intron-exon boundaries

A:Accession: A33321

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 16-66; 96; 121-159, 'D', '161-167 <AUE>

A:Note: these fragments represent a zinc finger-containing DNA-binding region

R:Gradwohl, G.; Menissier de Murcia, J.; Molinete, M.; Simonin, F.; Koken, M.; Hoeijmakers, J.H.J.; de Murcia, G.

Proc. Natl. Acad. Sci. U.S.A. 87, 2990-2994, 1990

A:Title: The second zinc-finger domain of poly(ADP-ribose) polymerase determines specificity for single-stranded breaks in DNA.

A:Reference number: A35635; MUID:90222155

A:Accession: A35635

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 12-26, 'T', '28-66; 116-166 <GRA>

R:Schneider, R.; Auer, B.; Kuehne, C.; Herzog, H.; Klocker, H.; Burtischer, H.; Hirsch-Kauffmann, M.; Wintersberger, U.; Schweiger, M.

Eur. J. Cell Biol. 44, 302-307, 1987

A:Title: Isolation of a cDNA clone for human NAD (+): protein ADP-ribosyltransferase.

A:Reference number: A61559; MUID:88082900

A:Accession: A61559

A:Molecule type: mRNA

A:Residues: 381-420; 682-710 <SCH>

R:Yokoyama, Y.; Kawamoto, T.; Mitsuuchi, Y.; Kurosaki, T.; Toda, K.; Ushiro, H.; Terashima, M.; Sumimoto, H.; Kuribayashi, I.; Yamamoto, Y.; Maeda, T.; Ikeda, H.; Sagara, Y.; Shizuta, Y.

Eur. J. Biochem. 194, 521-526, 1990

A:Title: Human poly(ADP-ribose) polymerase gene. Cloning of the promoter region.

A:Reference number: S14010; MUID:91099327

A:Accession: S14010

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-95 <YOK>

A:Cross-references: EMBL:X56140; NID:g35286; PIDN:CAA39606.1; PID:g825702

C:Comment: This protein can ADP-ribosylate itself as well as other proteins.

C:Genetics:

A:Gene: GDB:ADPRT; PPOL

A:Cross-references: GDB:119508; OMIM:173870

A:Map position: 1q41-lq42

C:Superfamily: NAD+ ADP-ribosyltransferase

C:Keywords: DNA binding; DNA repair; glycosyltransferase; NAD; nucleus; pentosyltransferase; zinc finger

A29725 Length: 1014 September 10, 2002 14:23 Type: P Check: 7353

MAESDLRYVEYAKSGRACCKCESIPKOSLRMAIMVQSPMFDGKVPWHVHSCFWKVGHSIRHPDVE

VDGSELDWDDQKVKYTAAGGVTKGQDGIKSKAEYKTLGDFAAEYAKSNRSTCKGMEKIEKQVRLS

KMDVDPQLQGMIDRWTHPGCFVKNRREELGFRPEYSASQLKFSLLATEDKEALKQLPGVKSGKRRG

DEVDPVQAKKKKSKDLKALQANDLIWNTKDELKVCSTNDKELIFNKKQVPSGSAIL

DRADQWVFALLPCEESGGLVFKSDAYCTGTAWTKCMVKTQTPNRKEWTPKFEISYGLKLV

KQDRIFPETSASVATPPSPASAAVSSADPLSNMKILTLGLKLSRNKDEKAMTEKLGKLT

TANKASICTIKKEVEKNKKMEVEKANIRVYSEDFLDQVSASTKSIQELFLAHILSPGAEVKAEPV

EWAPRGSGAALSKKSKQVKEGINKSERMKLTLGGAAYDPSDLSHSAHVLEKGGKVFSAITGLV

DIVKGTNYYKLQLEDDKENRYWIFRSWRTGVIGSKLEQMPSKEDAEHPMKLYEEKTGNAHWSKN

FTKYPKFEYPLEIDYGODEEAVKLTVPNGTKSKLPKVPQDLIKFMFVSGMKAMVEYEDLQKMLGK

LSKQIQAAYSITLSEVQQAQSGDSQILDSNRYFTLIPHDGKMPPLLNADSVQAKVEMLDNLD

LEVAYSLRGGSDSSKRPIDVNEKLTDKVVDSDSEAEIRKYVKNTHATTNAYDLEVIDFKIE

REGCORYKPKQLHNRLLHMGSRRTNFAGLISQGLRIAPPEAVTCYMGFGIYFADMYSKSNYCHT

SGQDPGILIGLGEVALGNMYELKASHLSKLPKGSVKHGLGKTPDPFSANISLDGVDVPLGTGTSGVN

DTSLLYNEYIYDIAQVNLKLLKLFNFKYSLMI

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; TOIG of: jh0581 check: 5006 from: 1 to: 1011
;
; P1: JH0581 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - chicken
; N: Alternate names: poly(ADP-ribose) synthase
; C: Species: Gallus gallus (chicken)
; C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
; C: Accession: JH0581
; R: Ittel, M.E.; Garnier, J.M.; Jeltsch, J.M.; Niedergang, C.P.
; Gene 102, 157-164, 1991
; A: Title: Chicken poly(ADP-ribose) synthetase: complete deduced amino acid
; sequence and comparison with mammalian enzyme sequences.
; A: Reference number: JH0581; MUID: 91340148
; A: Accession: JH0581
; A: Molecule type: mRNA
; A: Residues: 1-1011 <INT>
; A: Cross-references: EMBL:X52690; NID: g63742; PID: CAA36917.1; PID: g63743
; C: Comment: This protein is a chromatin-bound enzyme.
; C: Comment: This enzyme catalyzes DNA-dependent post-translational modifications
; of various nuclear proteins.
; C: Superfamily: NAD+ ADP-ribosyltransferase
; A: Title: Depression in gene expression for poly(ADP-ribose) synthetase during
; the interferon-gamma-induced activation process of murine macrophage tumor
; cells.
; C: Keywords: DNA binding; glycosyltransferase; NAD; nucleus;
; pentosyltransferase; zinc finger
;
; JH0581 Length: 1011 September 10, 2002 14:23 Type: P Check: 5006
; jh0581
; MAETGDKPYRAEYAKSGRASCCKGSGESIAKDSLRLALMVOSPMFDGKVPWHHYSCFWKRAIVSHSTDID
; GFPELRWDEOKIKKALETGALOPEKGTREKVGKAEKSLTDFAAEYAKSNRSTCKCEOKIEKGQIRIS
; KKVHPKPOLGMDINWYHDFCVSRRAEGLFLPAYATQLLGSILKADEKTEFLKKOLPAITEGRKRG
; EVDGVVAKKSRKEKESKOBKQKEQTELIWIKDELKVCSTNDLEKLLIANKEVPSGEGNAILD
; RVADGMAGFALLPCECKGQVFVKSDAYYCGSDITAWTKCAVQTPTNRKDWIPKREFRIPYLKFKCK
; KODRIFPEAATVNSAPPASAPLTETVTAPOQDKPLTNMKILTGLKSNKEVKVNIIEELGCKMTTAA
; NKATLCISTOKEVMKMKMEVEKDAKVRVVEEFLDKVSKNGFOELLSLHAI SPWGAEVKTEHOEVA
; VDGCSPKANKSAGKVEQGPSSKMKMLTVKGGAADPDSDGLEDSAHVPEKGGKIFSATLGLVDIV
; KGTNSYKLOLLEDDRESRYWVEFSWGRGTGVSNGKLEOMPSEKEDAVEHNLAYEKTGNSHRSKFTK
; YPKFYPEIDYGQDEAVAKGLSVSAGTKSLAKPIODLNMIFDVESMKKAMVEFIDLOKMPGLKSLK
; RQIOSAYSILNEVOQAVDGSQSLIDLRFTYLLPHDFGMKRPPLTHAENYIARQVMDNLLDIEV
; AYSLLRGNEGDGDKPIDINYEKLRTDIKVVDKSEAEKIKQYKVNTHAENYDLYKVEIFRIEREG
; ESQRYKPTKQLHNRLQHLHSGRTTNFAGILSGLRIAPPEAPVTGYMGFGKIYPRDMVKSANYCHTSSQA
; DPIGLILGELVALGNMYELKNASHITKLPKGKHSVKGLGKTAPDPTATTTLDGVEVPLNGISTGINDTC
; LLYNEYIYDYVAQVNLAYLLKLFNFKTSLW1
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; TOIG of: js0428 check: 8204 from: 1 to: 1016
;
; P1: JS0428 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - bovine
; N: Alternate names: ADP-ribosyltransferase (polymerizing); poly(adenosine
; diphosphate ribose) polymerase; poly(ADP-ribose) polymerase
; C: Species: Bos primigenius taurus (cattle)
; C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
; C: Accession: JS0428; S00328; A30458
; R: Saito, I.
; submitted to JIPID, February 1990
; A: Reference number: JS0428
; A: Accession: JS0428
; A: Molecule type: mRNA
; A: Residues: 1-1016 <SAI>
; A: Experimental source: thymus
; R: Taniguchi, T.; Yamauchi, K.; Yamamoto, T.; Toyoshima, K.; Harada, N.; Tanaka,
; H.; Takahashi, S.; Yamamoto, H.; Fujimoto, S.
; Eur. J. Biochem. 171, 571-575, 1988
; A: Title: Depression in gene expression for poly(ADP-ribose) synthetase during
; the interferon-gamma-induced activation process of murine macrophage tumor
; cells.
; A: Reference number: S00328; MUID: 88151954
; A: Accession: S00328
; A: Molecule type: mRNA
; A: Residues: 648-714; 838-904 <TAN>
; A: Cross-references: EMBL:X06986
; A: Accession: A30458
; A: Molecule type: protein
; A: Residues: 658-685; 689-696; 893-901 <TA2>
; C: Superfamily: NAD+ ADP-ribosyltransferase
; C: Keywords: DNA binding; glycosyltransferase; NAD; nucleotide binding; nucleus;
; P-loop; pentosyltransferase; zinc finger
; F: 21-51/Region: zinc finger
; F: 128-165/Region: zinc finger
; F: 200-220/Region: helix-turn-helix motif
; F: 224-231/Region: nuclear location signal
; F: 250-270/Region: helix-turn-helix motif
; F: 494-501/Region: nucleotide-binding motif A (P-loop)
; F: 890-903/Region: nucleotide binding #status predicted
;
; JS0428 Length: 1016 September 10, 2002 14:13 Type: P Check: 8204
; js0428
; MAESDKLYREYAKSGRASCCKKESIPKDSIRMAFVSPMFDGKIPHWIHLSCFWKVFSTIWHDPDE
; VEGFSELRWDDQOTIKKMAETGGRTDVSFGKGVGSKTEKTLIDFGAGYAKSNRSTCKSCMEKIDKQV
; RLKSKVVPDKPOLGMVDCWHPKCFVQKREELGFRPEFSATHLMGFSVLTAEDQETLKKOLPAIKGERK
; RKGDEVDGIDEVTKKSKKEKDEIKLEKALKAGNDLIWNVKDELKACSTNDLKELLINKNQVPSGES
; AILDRVADGMVFGALLPCEECGQLVFKGDIYCTGDVTATKCMVKTQTPNRKEWVTPKFEISIFKK
; LTKQDRIFPPESSTPVGAAPPASAPAAVHSPPDKPLSNMKILTGLKLSQNKDEKVKATIEKILGGK
; LTGTANKASLCISTKKEVDKLNKMEEVKEANIRVSEDFLODTSASTKLOELLSTHLISPMWGAEVKE
; PVEAVGPKGSGAAPSCKSKGPKVECTNKSEKRMKLTLSKGAADPDSDGLEHNAHLEKGGKVFSAITLG
; LVDIKGTNSYKLOLLEDDKESRYWIFRSKRGVTGVSNGKLEOMPSEKEDATIEHFMKLYEETGNAHWS
; KNTKHPKYPLEIDYGQDEEAVKLTVPNGTKSLKLPQVNLKIMIFDVESMKKAMVEFIDLOKMPDL
; GLSKRQIQIQAAYSILSEVOQALSGQSSDSHILDSNRFYTLIPHDFGMKRPPLTHAENYIARQVMDNLL
; LDIEVAYSLRGGSDSDSDPIDVNEKLTQDKVVDKSEAEIIRKYKVNTHAENYDLYKVEVDFIFK
; IERESQRYKPKFQLHNRLHSGRTTNFAGILSGLRIAPPEAPVTGYMGFGKIYFADWVSKSANYC
; HTSQGDDPIGLILGELVALGNMYELKHARHISKLPKGKHSVKGLGKTTPDPFSASITVDGVEVPLGTGISSG
; VNTECLLYNEYIYDYVAQVHLKYLKLFNFKTSLW1
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TOIG of: s26057 check: 8491 from: 1 to: 500

F1:S26057 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 18-Jun-1999

C:Accession: S26057; S78453; I52331

R:Thibodeau, J.; Gradwohl, G.; Dumas, C.; Clairoux-Moreau, S.; Brunet, G.; Penning, C.; Poirier, G.G.; Moreau, P.

Biochem. Cell Biol. 67, 653-660, 1989

A:Title: Cloning of rodent cDNA encoding the poly(ADP-ribose) polymerase catalytic domain and analysis of mRNA levels during the cell cycle.

A:Reference number: I52331; MUID:90027702

A:Accession: S26057

A:Molecule type: mRNA

A:Residues: 1-500 <THI>

A:Cross-references: EMBL:X65497; NID:g56849; PIDN:CAA46478.1; PID:g56850

R:Potvin, F.

submitted to the EMBL Data Library, March 1992

A:Reference number: S78453

A:Accession: S78453

A:Molecule type: mRNA

A:Residues: 1-124, 'H', 126-127, 'A', 129-238, 'D', 240-500 <POT>

A:Cross-references: EMBL:X65497

C:Superfamily: NAD+ ADP-ribosyltransferase

C:Keywords: DNA binding; DNA repair; glycosyltransferase; NAD; nucleus; pentosyltransferase

S26057 Length: 500 September 10, 2002 14:23 Type: P Check: 8491

GVNKSERMKLTLLKGAADVDPDGLSHSAHVLEKGGKVFSAITGLVDIVKGTNSYKQLLESDEKESRYW

IFRSWGRVGTIGNSLQMPKEDAVEHPMKLYEKTGNHWSKNFTKPKFYPLEIDYGDGEAVKK

LAVKPGTKSLPKVQLDLCMIFDVSMMKALVEYEDLQKPLKSRQIOAAYSILSEVQAVSQGS

SESQILDLSNRFYTLPHDFGKMKPPLNNNTDSQAVKEMLDNLDIEVAISLRLGSDSSKDPIDVNY

EKLKTDIKVVDROSEAEVIRKTVKNTHTATHNAYDLEVIDIEKIEREGESQRYKPPQJHNRLLWHGS

RTTNFAGILSQGLRIAPPEAPVTGYMFGGIYFADMVSKSANTCHTSQGDPIGLLILGEVALGNMYELKH

ASHISKLPGKHSVKGGLGTAPDPSASITLDGVEVPLGTGIPSGVNDTCLLYNEYIYVDIAQVNLKYLK

LKFNFTSLW1

TOIG of: s31735 check: 6153 from: 1 to: 998

F1:S31735 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - African clawed frog (fragment)

N:Alternate names: poly ADP-ribose polymerase

C:Species: Xenopus laevis (African clawed frog)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000

C:Accession: S31735; PN0495

R:Saulier-le Dreal, B.M.

submitted to the EMBL Data Library, May 1992

A:Reference number: S31735

A:Accession: S31735

A:Molecule type: mRNA

A:Residues: 1-998 <SAU>

A:Cross-references: EMBL:Z12139; NID:g64967; PIDN:CAA78126.1; PID:g1334661

R:Ozawa, Y.; Uchida, K.; Uchida, M.; Ani, Y.; Kushida, S.; Okada, N.; Miwa, M.

Biochem. Biophys. Res. Commun. 193, 119-125, 1993

A:Title: Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose)polymerase from Xenopus laevis and cherry salmon using heterologous oligonucleotide consensus sequences.

A:Reference number: PN0494; MUID:93277538

A:Accession: PN0495

A:Molecule type: mRNA

A:Residues: 742-745, 'E', 747-876 <OZA>

C:Superfamily: NAD+ ADP-ribosyltransferase

C:Keywords: DNA binding; glycosyltransferase; hexosyltransferase; NAD; nucleus; pentosyltransferase; zinc finger

S31735 Length: 998 September 10, 2002 14:22 Type: P Check: 6153

AKSGRACKKCGNIAKESLGLAIMVQSPMFDGKVPWHHYSFCWKRARVLSQGDYGYTELWEDQEMI

KKAIETGCGAAGAGDSKGGKEMTLNDFAAEYAKSNRSACKGCEQKIEKGQIRISKSVDPVLPQIGMI

DRYHPDGFVSREEDFLPSASQLKGTILSAEDKSLKKLPVKNKGRKADVDGHSAAATKKKI

KKEKESKLEKLLKEQTELIWHIKDELKKVCSTNDLKIANKQOVPSGETNIVDRVSDGMFAGALLP

CECSGQVFKGDAYCTGDSAWTKCAVKTQTPNRKDWTPKEFHEIPYLKKFKRHRARPPCAAPT

PISPRAAPEKPTVEETFPFGKPLTNTKVLIGLKNKDEVTLEIGLGGKVGASAKHNLCTSTNKEV

KMSKMEEVKAANRVVSDDFLKEVESGKSQVELLSQFGISWGAIEKQENAVQTEKQSPSPVAGKSS

GVKKEKSGNSKSEKMKLTVKGGAADPDSLEDSCHVLTGGKIFSAITGLVDITRGTNSYKQLDIEH

DRDSYVWFRSGRVGTIGSKLEEMSSKDAIEHFLNLYQDKTGNHWSNFTKPKFYPLEIDYGO

EEDVKKLSVAGTKSKLAPVQELIKLIFDVESMMKAMVEFEDLQKPLKSRQIQSAYSILSQVQ

QAVSELSSEARLLDSNOFYTLIPHDFGKMKPPLNNLEYIOAKVQMLDNLDEAVYSLRLGGADGEX

DPIDVKEKTKTDIKVYAKDSESRILICDVKNTHADTHNAYDLEVIDIEKIDREGEVQRYKPKQLHNR

QLLHSGSRTNFAGILSQGLRIAPPEAPVTGYMFGGIYFADMVSKSANTCHAMPSPGILGILLGEVALG

NMHELKAAASQITKLPKKGHSVKGGLGTAPDPSATVQDGDVDPVLPUGKTSANISDTSLLINEIYVDIAQV

NLKYLKLEKFNKGGMMW1

TOIG of: s42208 check: 1061 from: 1 to: 996
; P1:S42208 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - flesh fly (Sarcophaga
; peregrina)
; N:Alternate names: poly(ADP-ribose) polymerase
; C:Species: Sarcophaga peregrina
; C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
; C:Accession: S42208; S71496
; R:Masutani, M.; Nozaki, T.; Hitomi, Y.; Ikejima, M.; Nagasaki, K.; de Prati,
; A.C.; Kurata, S.; Natori, S.; Sugimura, T.; Esumi, H.
; Eur. J. Biochem. 220, 607-614, 1994
; A:Title: Cloning and functional expression of poly(ADP-ribose) polymerase cDNA
; from Sarcophaga peregrina.
; A:Reference number: S42208; MUID:94170813
; A:Accession: S42208
; A:Molecule type: mRNA
; A:Residues: 1-996 <MAS>
; A:Cross-references: EMBL:D16482; NID:g473742; PIDN:BAA03943.1; PID:g538248
; A:Accession: S71496
; A:Molecule type: protein
; A:Residues: 170-188; 721-736; 813-819; 879-885 <MAX>
; C:Superfamily: NAD+ ADP-ribosyltransferase
; C:Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc
; finger
; F:1-369/Domain: DNA binding #status predicted <DNA>
; F:370-507/Domain: auto-modification #status predicted <AMO>
; F:508-996/Domain: NAD binding #status predicted <NAD>
; S42208 Length: 996 September 10, 2002 14:23 Type: P Check: 1061
s42208
MEIDLFPKVEYSKSRASCKGNKIEAGILRIAAMVQSAPHDGKQPNWFHQCFQKQRPSTSGDIENF
ENIRFEDQIRKAIKIDNCTTVISAGSKLGRKSGENNAIKDFGIEYAKSRGSCGCEQRIKDKQIRI
RKTVDTEVMYGGPIWHVVECPAOLGELGLDGTGNLPGFOTLKSDDKADYKALPVIKDEGVSA
KKAKLEKIDEEAASIKELTEKIKQSKRLFRDEIKNEMSKDMDWALLEANNMPEYKGDSEKLLDQVA
DLUTFGALPCDTCGRQLLFHKSGLCLNGDLUTETWCKTLKEPERKSKIPGYLYKFLKDKVRKNPEV
RAIRYIPSTSLIKNISLKGDELDPKVRERPLNYNIEALIAKPERGIVKDRISKLGTVSTKIT
ERTVYVLTPEEVRMSRMKAKTIGLHVIPEDYLEAVEQNGAGAINYISSMLCDMGWTDPATRITQEE
SKSSKSKSYTKSPKSWTLKIDGLVADPDSGLDVAHVYVRNKEYNVVLGITDIQKNKNSFYKLQI
LESDMKNRFPWRSGRICTTIGGNKLDNFSNLVDALVQFKELYLEKSCNHFENRENVKVGAWYPIDI
DYAEQSKIDLAEHDKSKLPLSVQDILKLMFDVDSMKRTMWFEDLMEKHPGLKLSQKIQOSAYKVLTE
YIELQGGTNAFIDATNRFYTLPHNFQSPPLDITTEQVEQLRQMLDLIEIECAYSLLQTEDESKA
DINPIDKHVEQLTKLEPLDKNSEEYILQKYVKNTHAETHKLYDLEVVDIFPKVARQGEARRYKPKFLH
NRLLWHGSRLLTFAGILSHGLKIIAPPEAPVTGYMFGGIYFADVMVYSANTCCCTSHHNSLGLMLLSVA
LGMNMECTAAKYVTKLPNDKHKSCFCGRGRTMPNPSEIIREDCGVEIPLGKPIITNDSLKSLLYNEFIYDI
AQVNIQYMLRMNEKYKI

TOIG of: t01311 check: 5648 from: 1 to: 635
; P1:T01311 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - Arabidopsis thaliana
; N:Alternate names: poly(ADP-ribose) polymerase; protein T14P8.19
; C:Species: Arabidopsis thaliana (mouse-ear cress)
; C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
; C:Accession: T01311; S65662
; R:Kalicki, J.; Elliott, G.; Cloud, J.
; submitted to the EMBL Data Library, May 1998
; A:Description: The sequence of A. thaliana T14P8.
; A:Reference number: Z14290
; A:Accession: T01311
; A:Status: translated from GB/EMBL/DBJ
; A:Molecule type: DNA
; A:Residues: 1-635 <KAL>
; A:Cross-references: EMBL:AF069298; NID:g3193282; PID:g3193299
; A:Experimental source: cultivar Columbia
; R:Lepiniec, L.; Babiychuk, E.; Kushnir, S.; Van Montagu, M.; Inze, D.
; FEBS Lett. 364, 103-108, 1995
; A:Title: Characterization of an Arabidopsis thaliana cDNA homologue to animal
; poly(ADP-ribose) polymerase.
; A:Reference number: S65662; MUID:95269779
; A:Accession: S65662
; A:Status: nucleic acid sequence not shown
; A:Molecule type: mRNA
; A:Residues: 1-115, 'GT', 116-635 <LEP>
; A:Cross-references: EMBL:248243; NID:g853721; PIDN:CAA88288.1; PID:g853722
; C:Genetics:
; A:Gene: PARP
; A:Map position: 4
; A:Introns: 28/3; 116/1; 162/3; 190/1; 268/3; 312/1; 330/3; 355/2; 371/1; 387/3;
; 408/3; 435/3; 472/3; 498/1; 545/3; 570/2; 605/3
; A:Note: T14P8.19
; C:Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc
; finger
; T01311 Length: 635 September 10, 2002 14:13 Type: P Check: 5648
t01311
MANKLVDELRLKLAERGLSTGVKAVLVERLEEIAEDTKKEESKSKRKNSSNDTVESNKLIAIGFER
GMIVRELBEAIKRGDITGTIGKDLRLCDANNVSNAPVKSNDDEADDNNGFEERKEKIVTATKK
GAALVDQPIDEIKSQYHVLQGGDDYDALNQTNRNNKFFVLQLESDSKTYTVYTWGRGVKVG
QSKLDGPYDSWDRAIEITFNKNDKTYNSDRKEIFPHKSYTWLEMDYKGEENDSPVNNIPSSSEV
KPEQSKLDTYAKFTSLICNYSMAQHMWEGYGNANKPLGKISKSTISKGVEVLKRISVIDRYDTRL
BELSGEFTYVPHDFGFKMSQFVDTTPQKLKQKTEMVEALGEIELATKLLSVDPGLQDDPLYHYHQTLN
CGLTVPQNDSEESFVSANYMENTHAKTHSGYTVETIAQLFRASRAVEADRFQOFSSKKNMLLWHGSRLTN
WAGILSQGLRTAPPEAPVTGMFGKGVTFADMFSAKSNCTANTGANDGVLLCEVALGDMNELLYSYDN
ADNLPPGKLSTKGVGKGTAPNPSEAOQLDEGVVVVPLGKPKVRSCKSGMLLYNEYIVNVEQIKMRYIOVK
FNKHI

```
! FINDPATTERNS on *.pir* allowing 0 mismatches
!
1 CXXCX{28,30}HXXC          September 10, 2002 14:25 ..

a29725.pir1 ck: 7353 len: 1,014 ! P1:A29725 - NAD+ ADP-ribosyltransferase (EC
1 CXXCX{28,30}HXXC
  CXXCX{28}HxxC
21: SGRAS CKKSESIIPKDSLRLAIVQSPMFDGKVPWHYHFSC FWKVG
  CXXCX{30}HxxC
125: SNRST CKGMEKIEKGQVRLSKMVDPEKPOLGMIDRWYHPGC FVKNR

jh0581.pir1 ck: 5006 len: 1,011 ! P1:JH0581 - NAD+ ADP-ribosyltransferase (EC
1 CXXCX{28,30}HXXC
  CXXCX{28}HxxC
21: SGRAS CKKGESIAKDSLRLALMVQSPMFDGKVPWHHHYSC FWKRA
  CXXCX{30}HxxC
125: SNRST CKGCEQIEKGQIRISKMWHPKXPQLGMIDNWIHPDC FVSRR

js0428.pir1 ck: 8204 len: 1,016 ! P1:JS0428 - NAD+ ADP-ribosyltransferase (EC
1 CXXCX{28,30}HXXC
  CXXCX{28}HxxC
21: SGRAS CKKCKESIPKDSIRMAFVESPMDGKIPWHYHLSC FWKVG
  CXXCX{30}HxxC
128: SNRST CKSCMEKIDKGQVRLSKKVYVPDKPOLGMVDCWYHPKC FVQKR

s31735.pir2 ck: 6153 len: 998 ! F1:S31735 - NAD+ ADP-ribosyltransferase (EC
1 CXXCX{28,30}HXXC
  CXXCX{28}HxxC
8: SGRAS CKKCGDNIAKESLGLAIVQSPMFDGKVPWHHHYSC FWKRA
  CXXCX{30}HxxC
111: SNRSA CKGCEQIEKGQIRISKSDVERPOLGMIDRWYHPDC FVSSR

s42208.pir1 ck: 1061 len: 996 ! P1:S42208 - NAD+ ADP-ribosyltransferase (EC
1 CXXCX{28,30}HXXC
  CXXCX{28}HxxC
19: SSRAS CKGCKNIEAGILRIAAMVQSAFHDGKQPNWFHEQC FFQKQ
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Total finds:          9
Total length:        6,170
Total sequences:      7
CPU time:            00.04
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TOIG of: aar99642 check: 3219 from: 1 to: 1013
ID AAR99642 standard; Protein; 1013 AA.
AC AAR99642;
XX
XX 31-OCT-1996 (first entry)
XX
XX Poly(ADP-ribose) polymerase contg. DNA-binding domain.
XX
XX PARP; DNA-binding domain; poly(ADP-ribose) polymerase; gene therapy;
XX tumour treatment; DNA repair; over-expression.
XX
XX Homo sapiens.
XX
XX WO9618737-A2.
XX
XX PN 20-JUN-1996.
XX
XX PD 15-DEC-1995; 95WO-DE01817.
XX
XX PF 16-DEC-1994; 94DE-4444949.
XX
XX PR (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX PA Buerkle A, Kuepper J, Zur Hausen H;
XX
XX PI WPI: 1996-300654/30.
XX
XX DR N-PSDB; AAT13732.
XX
XX DX Vectors contg. insert encoding DNA-binding domain of
XX poly(ADP-ribose) polymerase - useful for gene therapy, esp. of
XX tumours
XX
XX PS Disclosure; Fig 1; 22pp; German.
XX
XX CC The present sequence is that of a poly(ADP-ribose) polymerase (PARP)
XX contg. a DNA-binding domain (DBD). It is encoded by AAT13732, from
XX which a fragment comprising nucleotides 67-1220 (-29 to +1127) encoding
XX the DBD can be inserted into vectors which are used for gene therapy.
XX Over-expression of the DBD inhibits the DNA repair function of PARP, so
XX the vectors are useful for gene therapy or tumours, esp. in combination
XX with conventional chemo- and/or radiotherapy.
XX
XX SQ Sequence 1013 AA;
AAR99642 Length: 1013 September 10, 2002 14:39 Type: P Check: 3219
aar99642
MAESSDKLYRYEAKSERACKSCSEIPKDSLRMAIMVQSPMFGKVPWHYHFCFWKVGHSIRHPDVE
VDFSELWDQOQVKTAEAGVGTGQDGIGSKAEKTLGDFAAEYAKNRSTCKGCMKIEKGQVRLS
KMVDPEKPOLGMDIRWYHPCGVKNGREELGFRPEYSASOLKGFSLATKEDKALKKOLPGVSEGRKRG
KDVGDEVAKKSKKEKDKSKLEKRLKQNDLWIKRDELKVKCSTNDLKELLIFNKQOVPSGSAIL
DRVADGVGALLPCSECSQVFKSDAYTCGTGTAWTKCMVKTQTPNKRKWTPEFREISYLKLLAV
KKQDRIFPPTSASVAHPPTASAPAAVNSSASADKPLSNMKLTGLKLSRNKDEKAMIEKLGKLTG
TANKSLCTSTKEVEKMNMKEVEKAEANRVVSEDFLDQVASTKSLQFLFLAHILSPMGAEVKAEPVE
VAPRGKSAALSKSGQVKEGINKSEKMKLTGKGAAPDPSGLEHSAHLEKGGKVSATLGLVD
IVKGTNSYKQLLEDKERNYVIFRSWGRVTVIGSNLEQMPKSEDAIEHPMKLYEERTGNAMHSKNF
TKYPKFPLEIDYGODEAVKLTIVNPGTKSLPKPVODLIKIFDVESMKKAMVEYEDLQKPLGKL
SKQIOANVLSILEVQVQVSGSSDQLDLSNRFYTLPHDFGMRKPPLLNNADSVQAKVEMDLNLDI
EVAILSGGSDSDSKDDIDVNETKLTDLKVVDRDSEAEIIRKYVKNTHATTHAYDLVIDIFKIER
EGECQRYKPKQLHNRRLNLFNAGILSQGLRIAPPEAPVTGYMGFGIYFADMYSKSANTCHTS
QGDPILGILGLGEVALGNMVELKHAHISKLPGKHSVKGGLGKTTDPSPANSISLDGVDVPLGTGTSISGVND
TSLLYNEYIVDYAQVNLKYLKLFNFKTSLW1

TOIG of: aay68834 check: 7074 from: 1 to: 653
ID AAY68834 standard; Protein; 653 AA.
XX
XX AC AAY68834;
XX
XX DT 16-MAY-2000 (first entry)
XX
XX DE A poly(ADP-ribose) polymerase NAP protein of Zea mays.
XX
XX KW NAP; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase;
XX programmed cell death; apoptosis; growth rate; stress; cold; pathogen;
XX pest; drought; heat; fungi; nematode; seed-shatter.
XX
XX OS Zea mays.
XX
XX PN Key Location/Qualifiers
XX FT Misc-difference 1..159 /note="these residues are specifically claimed in
XX ET Claim 18"
XX
XX PN WO200004173-A1.
XX
XX PD 27-JAN-2000.
XX
XX PF 12-JUL-1999; 99WO-EP04940.
XX
XX PR 17-JUL-1998; 98US-0118276.
XX
XX PA (PLBZ) PLANT GENETIC SYSTEMS NV.
XX
XX PI Babychuk E, Kushnir S, De Block M;
XX
XX DR WPI: 2000-182436/16.
XX
XX DR N-PSDB; AAZ60616.
XX
XX PT Modulating cell death, growth and stress resistance in eukaryotes,
XX specifically plants, used, e.g. to impart fungus or nematode resistance
XX
XX PS Claim 18; Page 92-95; 126pp; English.
XX
XX CC The present sequence represents the NAP protein of Zea mays. This
XX protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as
XX poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed
XX cell death or apoptosis, and is a nuclear enzyme. The NAP polynucleotide
XX sequences can be used for modulation of programmed cell death in
XX eukaryotic cells. The method is used, specifically in plants, to induce,
XX or protect against, programmed cell death, depending on the extent to
XX which PARP activity is reduced. Reducing expression of endogenous NAP
XX class PARP only is also used to modulate programmed cell death, to
XX increase growth rate and to produce plant cells that are more tolerant
XX of stress (cold, chemical treatments, pathogens, pests, drought, heat,
XX etc., or during transformation). Particular applications are generation
XX of plants that are resistant to fungi or nematodes; are male or female
XX sterile; or have better seed-shatter properties. The methods are also
XX used to improve growth of transformed plant cells (and derived calli or
XX complete plants).
XX
XX SQ Sequence 653 AA;
AAY68834 Length: 653 September 10, 2002 14:38 Type: P Check: 7074
aay68834
MSARLRVRAELQRLDVSCTKALVRRLLDAACEAKVAAAPTAVANGVAVDGRKNCGNKR
KRSDDGEEGNDTCTDVTKLEGSYRELQAKARGAAANGKKDVIOQLLSATGAPAAVADGGPLGAK
EVIKGGDEEVKVKERKMTATKGAALVDQHIYHVLQVGDIEYDATTNQTVNGDNNKFYIIQ
VLESDAGGSFMYNRWGRVGRQDQLHGSPTRDQAIYEFEGKFNKTNHNSDRKNFCYAKYTWLE
MDYGETEKETKGSITDOLKETLETRIAQFISLIGNSMKORMVEIGYNAEKLPLGKLRKATILKGYH
VLKRI SDVTSKADRRHLEQLTGEYTVIPIPHDFGRKMRFIIDTPQKLKAKLEKVEALGEGIEATLKLED
DSSDDQDDPLYARKQLHCDFTPLEADSDSEYSMTKSYLRNTHGTHSGYTVDI VOIFKVSRHGETERPKQ
ASTRNRLMLHWSRLSNWAGILSQGLRIAPPEAPVTGYMGFGIYFADMYSKSANTCHTS
CEVALGDMNELLNADYDANLPRKLRKSGVGTAPNWNVESKVADDDVVVYVPLGEPKQPSKRGGLLYNEY

IVNVNQIRRMRYVLHVNFKRR1

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! FINDPATTERNS on *.geneseq* allowing 0 mismatches
!      1 CXXCX[28,30]HXXC      September 10, 2002 14:41 ..
aar99642.geneseqp1990s ck: 3219 len: 1,013 ! ID  AAR99642 standard; Protein; 1013 AA
1      CXXCX[28,30]HXXC
      CXXCX[28]HxxC
21: SERAS CKKCESEIPKDSLRMAIMVQSPMFDGKVPDHWYHFSC FWKVG
      CxxCx[30]HxxC
125: SNRST CKGCMKIEKGQRLSKKMDPEKPKLGMDRWHYHPC FVKNR

Total finds:      2
Total length:    1,666
Total sequences:  2
CPU time:        00.02
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